



## SEQUENCE LISTING

<110> DARST, SETH A.  
CAMPBELL, ELIZABETH

<120> A CRYSTAL OF BACTERIAL CORE RNA POLYMERASE WITH  
RIFAMPICIN AND METHODS OF USE THEREOF

<130> IPT-012.02

<140> 10/783,206  
<141> 2004-02-20

<150> 09/802,755  
<151> 2001-03-09

<160> 30

<170> PatentIn Ver. 3.2

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<213> *Thermus aquaticus*

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35 40 45  
Ile Phe Gly Pro Ile Lys Asp Tyr Glu Cys Ala Cys Gly Lys Tyr Lys  
50 55 60  
Arg Gln Arg Phe Glu Gly Lys Val Cys Glu Arg Cys Gly Val Glu Val  
65 70 75 80  
Thr Arg Ser Ile Val Arg Arg Tyr Arg Met Gly His Ile Glu Leu Ala  
85 90 95  
Thr Pro Ala Ala His Ile Trp Phe Val Lys Asp Val Pro Ser Lys Ile  
100 105 110  
Gly Thr Leu Leu Asp Leu Phe Ala Thr Glu Leu Glu Gln Val Leu Tyr  
115 120 125  
Phe Asn Lys Tyr Ile Val Leu Asp Pro Lys Gly Ala Val Leu Asp Gly  
130 135 140

Val	Pro	Val	Glu	Lys	Arg	Gln	Leu	Leu	Thr	Asp	Glu	Glu	Tyr	Arg	Glu	145	150	155			160
Leu	Arg	Tyr	Gly	Lys	Gln	Glu	Thr	Tyr	Pro	Leu	Pro	Ala	Gly	Val	Asp		165	170			175
Ala	Leu	Val	Lys	Asp	Gly	Glu	Glu	Val	Val	Lys	Gly	Gln	Glu	Leu	Ala		180	185			190
Pro	Gly	Val	Val	Ser	Arg	Met	Asp	Gly	Val	Gly	Ser	Leu	Pro	Leu	Pro		195	200			205
Arg	Arg	Val	Arg	Val	Asp	Tyr	Leu	Arg	Lys	Glu	Arg	Ala	Ala	Leu	Arg		210	215			220
Ile	Pro	Leu	Ser	Ala	Trp	Val	Glu	Lys	Glu	Pro	Tyr	Arg	Pro	Gly	Glu		225	230			235
Val	Leu	Ala	Glu	Leu	Ser	Glu	Pro	Tyr	Leu	Phe	Arg	Ala	Glu	Glu	Ser		245	250			255
Gly	Val	Val	Glu	Leu	Lys	Asp	Leu	Ala	Glu	Gly	His	Leu	Ile	Tyr	Leu		260	265			270
Arg	Gln	Glu	Glu	Glu	Val	Val	Ala	Arg	Tyr	Phe	Leu	Pro	Ala	Gly	Met		275	280			285
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Ala	Glu	Gly	Lys	Gly	Leu	Leu	Arg	Leu	Pro	Arg	His	Met	Thr	Ala	Lys		305	310			315
Glu	Val	Glu	Ala	Glu	Glu	Glu	Gly	Asp	Ser	Val	His	Leu	Thr	Leu	Phe		325	330			335
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Tyr	Pro	Phe	Glu	Asp	Asp	Val	Glu	Val	Thr	Thr	Gly	Asp	Arg	Val	Ala		405	410			415
Pro	Gly	Asp	Val	Leu	Ala	Asp	Gly	Gly	Lys	Val	Lys	Ser	Glu	Ile	Tyr		420	425			430
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Ser Tyr Asp Ile Asp Ala Arg Met Gly Ala Glu Ala Ile Gln Glu Leu  
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 Met Lys His Pro Ser Arg Ala Arg Arg Ala Lys Ala Arg Lys Arg Leu  
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 Glu Val Val Arg Ala Phe Leu Asp Ser Gly Asn Arg Pro Glu Trp Met  
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 Tyr Ser Gly Arg Ser Val Ile Val Val Gly Pro Gln Leu Lys Leu His  
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 850 855 860  
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 Lys Arg Ser Asp Ile Glu Ser Gly Leu Tyr Gly Arg Val Leu Ala Arg  
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 1315 1320 1325  
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          20              25              30

Asp  Val  Pro  Pro  Glu  Lys  Arg  Glu  Asn  Val  Gly  Ile  Gln  Ala  Ala  Phe
          35              40              45

Lys  Glu  Thr  Phe  Pro  Ile  Glu  Glu  Gly  Asp  Lys  Gly  Lys  Gly  Gly  Leu
  50              55              60

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Val	Leu	Asp	Phe	Leu	Glu	Tyr	Arg	Ile	Gly	Asp	Pro	Pro	Phe	Ser	Gln	65	70	75	80
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Arg	Leu	Gln	Leu	Ile	His	Lys	Asp	Thr	Gly	Leu	Ile	Lys	Glu	Asp	Glu	100	105	110	
Val	Phe	Leu	Gly	His	Leu	Pro	Leu	Met	Thr	Glu	Asp	Gly	Ser	Phe	Ile	115	120	125	
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Gly	Val	Tyr	Phe	Thr	Pro	Asp	Pro	Ala	Arg	Pro	Gly	Arg	Tyr	Ile	Ala	145	150	155	160
Ser	Ile	Ile	Pro	Leu	Pro	Lys	Arg	Gly	Pro	Trp	Ile	Asp	Leu	Glu	Val	165	170	175	
Glu	Ala	Ser	Gly	Val	Val	Thr	Met	Lys	Val	Asn	Lys	Arg	Lys	Phe	Pro	180	185	190	
Leu	Val	Leu	Leu	Leu	Arg	Val	Leu	Gly	Tyr	Asp	Gln	Glu	Thr	Leu	Val	195	200	205	
Arg	Glu	Leu	Ser	Ala	Tyr	Gly	Asp	Leu	Val	Gln	Gly	Leu	Leu	Asp	Glu	210	215	220	
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Gly	Arg	Tyr	Lys	Ala	Glu	Glu	Lys	Leu	Gly	Val	Gly	Leu	Ser	Gly	Arg	275	280	285	
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Pro	Thr	Leu	Arg	Tyr	Leu	Phe	Ala	Leu	Thr	Ala	Gly	Val	Pro	Gly	His	305	310	315	320
Glu	Val	Asp	Asp	Ile	Asp	His	Leu	Gly	Asn	Arg	Arg	Ile	Arg	Thr	Val	325	330	335	
Gly	Glu	Leu	Met	Ala	Asp	Gln	Phe	Arg	Val	Gly	Leu	Ala	Arg	Leu	Ala	340	345	350	
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Pro Ala Lys Leu Val Asn Ser Arg Pro Leu Glu Ala Ala Leu Arg Glu  
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 Leu Ser Ser Leu Arg His Lys Arg Arg Ile Ser Ala Leu Gly Pro Gly  
 405 410 415  
 Gly Leu Thr Arg Glu Arg Ala Gly Phe Asp Val Arg Asp Val His Arg  
 420 425 430  
 Thr His Tyr Gly Arg Ile Cys Pro Val Glu Thr Pro Glu Gly Ala Asn  
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 485 490 495  
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 580 585 590  
 Ala Ala Leu Tyr Ala Glu Glu Asp Gly Glu Val Val Lys Val Asp Gly  
 595 600 605  
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 610 615 620  
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 Asp Gly Pro Ala Ser Glu Glu Gly Phe Leu Ala Leu Gly Gln Asn Val  
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Val	Ile	Ser	Glu	Glu	Leu	Xaa	Xaa	Arg	Asp	Phe	Tyr	Thr	Ser	Ile	His		
		690				695					700						
Ile	Glu	Arg	Tyr	Glu	Ile	Glu	Ala	Arg	Asp	Thr	Lys	Leu	Gly	Pro	Glu		
705					710					715					720		
Arg	Ile	Thr	Arg	Asp	Ile	Pro	His	Leu	Ser	Glu	Ala	Ala	Leu	Arg	Asp		
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Leu	Asp	Glu	Glu	Gly	Ile	Val	Arg	Ile	Gly	Ala	Glu	Val	Lys	Pro	Gly		
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Asp	Ile	Leu	Val	Gly	Arg	Thr	Ser	Phe	Lys	Gly	Glu	Gln	Glu	Pro	Ser		
		755					760					765					
Pro	Glu	Glu	Arg	Leu	Leu	Arg	Ser	Ile	Phe	Gly	Glu	Lys	Ala	Arg	Asp		
		770				775					780						
Val	Lys	Asp	Thr	Ser	Leu	Arg	Val	Pro	Pro	Gly	Glu	Gly	Gly	Ile	Val		
785					790					795					800		
Val	Gly	Arg	Leu	Arg	Leu	Arg	Arg	Gly	Asp	Pro	Gly	Val	Glu	Leu	Lys		
			805						810					815			
Pro	Gly	Val	Arg	Glu	Val	Val	Arg	Val	Phe	Val	Ala	Gln	Lys	Arg	Lys		
			820					825					830				
Leu	Gln	Val	Gly	Asp	Lys	Leu	Ala	Asn	Arg	His	Gly	Asn	Lys	Gly	Val		
		835					840					845					
Val	Ala	Lys	Ile	Leu	Pro	Val	Glu	Asp	Met	Pro	His	Leu	Pro	Asp	Gly		
		850				855					860						
Thr	Pro	Val	Asp	Val	Ile	Leu	Asn	Pro	Leu	Gly	Val	Pro	Ser	Arg	Met		
865					870					875					880		
Asn	Leu	Gly	Gln	Ile	Leu	Glu	Thr	His	Leu	Gly	Leu	Ala	Gly	Tyr	Phe		
				885					890					895			
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			900					905					910				
Glu	Ile	Lys	Glu	Leu	Leu	Ala	Glu	Ala	Phe	Asn	Leu	Tyr	Phe	Gly	Lys		
		915					920					925					
Arg	Gln	Gly	Glu	Gly	Phe	Gly	Val	Asp	Lys	Arg	Glu	Lys	Glu	Val	Leu		
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Ala	Arg	Ala	Glu	Lys	Leu	Gly	Leu	Val	Ser	Pro	Gly	Lys	Ser	Pro	Glu		
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 Pro Gly Thr Ala Val Thr Ser Val Tyr Ile Glu Asp Val Leu His Glu  
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 Phe Ser Thr Ile Pro Gly Val Lys Glu Asp Val Val Glu Ile Ile Leu  
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35 40 45

Arg Thr Leu Glu Gly Leu Tyr Asp Asp Pro Asn Ala Val Thr Trp Ala  
50 55 60

Met Lys Glu Leu Leu Thr Gly Arg Leu Phe Phe Gly Glu Asn Leu Val  
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<222> (11)  
<223> Met, Ile or Val

<220>  
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<222> (12)  
<223> Asp, Val, Tyr, Glu, Gly or Ala

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<221> MOD\_RES  
<222> (14)  
<223> Asn or His

<220>  
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<223> Leu or Met

<220>  
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<222> (18)  
<223> Ser or Leu

<220>  
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<223> Thr, Cys, Gly or Asn

<220>  
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<223> His, Tyr, Asp, Arg, Leu or Pro

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<222> (23)  
<223> Lys, Thr, Gln or Glu

<220>  
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<222> (28)  
<223> Ser, Leu, Trp, Cys, Gln, or Tyr

<220>  
<221> MOD\_RES  
<222> (30)  
<223> Leu or Pro



&lt;400&gt; 14

Phe Phe Xaa Thr Ser Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gln Xaa Asn Pro  
 1 5 10 15

Xaa Xaa Gly Leu Xaa Xaa Xaa Arg Arg Asn Leu Xaa Ala Xaa Gly Pro  
 20 25 30

Gly Gly

&lt;210&gt; 15

&lt;211&gt; 14

&lt;212&gt; PRT

&lt;213&gt; Mycobacterium tuberculosis

&lt;400&gt; 15

Glu Thr Pro Glu Gly Pro Asn Ile Gly Leu Ile Gly Ser Leu  
 1 5 10

&lt;210&gt; 16

&lt;211&gt; 7

&lt;212&gt; PRT

&lt;213&gt; Mycobacterium tuberculosis

&lt;400&gt; 16

Asn Met Gln Arg Gln Ala Val  
 1 5

&lt;210&gt; 17

&lt;211&gt; 6

&lt;212&gt; PRT

&lt;213&gt; Saccharomyces cerevisiae

&lt;400&gt; 17

Lys Val Leu Ile Ala Gln  
 1 5

&lt;210&gt; 18

&lt;211&gt; 31

&lt;212&gt; PRT

&lt;213&gt; Saccharomyces cerevisiae

&lt;400&gt; 18

Met Ser Ser Arg Ala Gly Val Ser Gln Val Leu Asn Arg Tyr Thr Tyr  
 1 5 10 15

Ser Ser Thr Leu Ser His Leu Arg Arg Thr Asn Thr Pro Ile Gly  
 20 25 30

&lt;210&gt; 19

&lt;211&gt; 14

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 19

Glu Thr Pro Glu Gly Gln Ala Cys Gly Leu Val Lys Asn Leu  
1 5 10

<210> 20

<211> 7

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 20

Ala Met Gly Lys Gln Ala Met  
1 5

<210> 21

<211> 6

<212> PRT

<213> *Homo sapiens*

<400> 21

Lys Val Leu Ile Ala Gln  
1 5

<210> 22

<211> 31

<212> PRT

<213> *Homo sapiens*

<400> 22

His Gln Ala Arg Ala Gly Val Ser Gln Val Leu Asn Arg Leu Thr Phe  
1 5 10 15

Ala Ser Thr Leu Ser His Leu Arg Arg Leu Asn Ser Pro Ile Gly  
20 25 30

<210> 23

<211> 14

<212> PRT

<213> *Homo sapiens*

<400> 23

Glu Thr Pro Glu Gly His Ala Val Gly Leu Val Lys Asn Leu  
1 5 10

<210> 24

<211> 7

<212> PRT

<213> *Homo sapiens*

&lt;400&gt; 24

Ala Met Gly Lys Gln Ala Met

1

5

&lt;210&gt; 25

&lt;211&gt; 6

&lt;212&gt; PRT

<213> *Drosophila melanogaster*

&lt;400&gt; 25

Lys Val Leu Ile Ala Gln

1

5

&lt;210&gt; 26

&lt;211&gt; 31

&lt;212&gt; PRT

<213> *Drosophila melanogaster*

&lt;400&gt; 26

His Gln Ala Arg Ala Gly Val Ser Gln Val Leu Asn Arg Leu Thr Phe

1

5

10

15

Ala Ser Thr Leu Ser His Leu Arg Arg Val Asn Ser Pro Ile Gly

20

25

30

&lt;210&gt; 27

&lt;211&gt; 14

&lt;212&gt; PRT

<213> *Drosophila melanogaster*

&lt;400&gt; 27

Glu Thr Pro Glu Gly Ala Ala Val Gly Leu Val Lys Asn Leu

1

5

10

&lt;210&gt; 28

&lt;211&gt; 7

&lt;212&gt; PRT

<213> *Drosophila melanogaster*

&lt;400&gt; 28

Ala Met Gly Lys Gln Ala Met

1

5

&lt;210&gt; 29

&lt;211&gt; 4

&lt;212&gt; PRT

<213> *Escherichia coli*

&lt;400&gt; 29

Tyr Trp Ile Val

1

<210> 30

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
polynucleotide sequence

<400> 30

tgaaattgtc ggcgattta

19